

Run on:	July 18, 2001, 08:36:35 ; Search time 16:52 Seconds							
Copyright: (c) 1993 - 2000 Compugen Ltd.	Gencore version 4.5							
OM protein - protein search, using sw model								
Title:	US-09-502-176-2							
Perfect score:	1540							
Sequence:	I VYLSCKRTGNGKKNYRGTMSK. .... TNSQVRWEYCKIPSCDSSPV 260							
Scoring table:	BLOSUM62							
Sequenced:	Gapop 10.0 , Gapext 0.5							
Total number of hits satisfying chosen parameters:	219241							
Minimum DB seq length:	0							
Maximum DB seq length:	200000000							
Post-processing:	Maximum Match 0%							
Database :	Listing first 45 summaries							
PIR_68:*								
1: pir1:*								
2: pir2:*								
3: pir3:*								
4: pir4:*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	219241							
Result No.	Score	Query	%	Match Length	DB	ID	Description	
SUMMARIES								
1	1535	99.7	810	1	PLHU		RESULT 1	
2	1442	93.6	810	2	B30848		PLHU	
3	1292	83.9	790	1	PLPG		plasmin (EC 3.4.21.7) precursor [validated] - human	
	1291	83.8	812	1	PLBO		N;Alternate names: plasminogen precursor [mismomer]	
	1274	82.7	812	1	PLMS		N;Contains: angiotensin; microplasmin; plasminogen	
	1237	80.3	810	2	I46260		C;Species: Homo sapiens (man)	
	881	57.2	2869	1	I81851		C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000	
	879	51.8	728	1	JH0579		C;Accession: A35229; I5229; B26646; 16238; 184609; S03735; A00929; A04627; A04625;	
	9	782	50.8	728	1	A35644		R;Petersen, T.E.; Martz, M.R.; Ichinose, A.; Davie, E.W.
	10	764	50.4	710	1	A60185		J. Biol. Chem. 265, 6104-6111, 1990
	11	776	50.4	728	1	A60185		A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the f
	12	766.5	49.8	716	1	JC5061		A;Reference number: A35229; MUID:9020879
	13	754.5	49.0	411	2	A40332		A;Molecule type: DNA
	14	753.5	48.9	716	1	S00657		A;Accession: A26646; MUID:87162490
	15	749	48.6	4548	1	A41735		A;Molecule type: mRNA
	16	739	48.0	711	1	A32869		A;Residues: 1-471, 'D', 473-810 <FOR>
	17	739	48.0	1420	2	A32869		A;Cross-references: GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531
	18	505	45.5	455	2	A61545		A;Experimental source: Liver
	19	49.9	450	411	2	B61545		R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
	20	391.5	48.9	516	1	S33879		Biochemistry 23, 4243-4250, 1984
	21	372	24.2	625	1	TBBO		A;Title: Characterization of a complementary deoxyribonucleic acid coding for human a
	22	362.5	23.5	169	1	A40522		A;Reference number: I45961; MUID:85023311
	23	357.5	23.2	618	2	A35827		A;Accession: I62738
	24	351	32.8	455	2	A61545		A;Status: translated from GB/EMBL/DBDJ
	25	348	32.4	460	2	B61545		A;Molecule type: mRNA
	26	309.5	22.6	617	2	S10511		A;Residues: 367-419 <MAL2>
	27	295.5	19.2	559	1	UKHUT		A;Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:9387031
	28	281.5	18.3	559	1	A35029		R;Brundisholz, R.A.; Larch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, E.;J. Biochem. 114, 465-470, 1981
	29	278	18.1	120	2	A29941		A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

A; Reference number: S03735; MUID:81212097	A; Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
A; Molecule type: protein	R; Padmanabhan, K.; Tulinsky, A.
A; Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	submitted to the Brookhaven Protein Data Bank, April 1994
R; Wiman, B.; Petersen, T.E.; Magnusson, S.	A; Reference number: A52408; PDB:1PKK
submitted to the Attilas, July 1977	R; Contests: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
A; Reference number: A00929	R; Tulinsky, A.; Mathews, I.I.
A; Reference number: A00929	submitted to the Brookhaven Protein Data Bank, December 1995
A; Molecule type: protein	R; Reference number: A65244; PDB:1EKA
A; Residues: 501-810 <WII>	A; Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R; Wiman, B.; Wallen, P.	R; Tulinsky, A.; Mathews, I.I.
Eur. J. Biochem. 76, 129-137, 1977	submitted to the Brookhaven Protein Data Bank, December 1995
A; Title: Primary structure of the B-chain of human plasmin.	R; Tulinsky, A.; Mathews, I.I.
A; Reference number: A04627; MUID:77225245	submitted to the Brookhaven Protein Data Bank, December 1995
A; Accession: A04627	R; Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
A; Molecule type: protein	Biochemistry 30, 10576-10588, 1991
A; Residues: 501-810 <WII>	A; Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.5
R; Wiman, B.; Wallen, P.	A; Reference number: A58819; MUID:92031502
Eur. J. Biochem. 50, 489-494, 1975	A; Contents: annotation
A; Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen.	R; Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
A; Reference number: A04625; MUID:75093329	Biochemistry 30, 10589-10594, 1991
A; Accession: A04625	A; Title: The refined structure of the epsilon-aminocaproic acid complex of human plasminogen.
A; Molecule type: protein	A; Reference number: A58818; MUID:92031503
A; Residues: 20-50, 'O', 51-71, 'E', 73-85, 87-100 <WII2>	A; Contents: annotation
R; Wiman, B.; Wallen, P.	R; de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, K.
Eur. J. Biochem. 58, 539-547, 1975	Biochemistry 31, 270-279, 1992
A; Title: Amino-acid sequence of the cyanogen-bronide fragment from human plasminogen that	A; Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.1 angstroms.
A; Reference number: A04626; MUID:76043692	A; Reference number: A39433; MUID:92118803
A; Accession: A04626	A; Contents: annotation; X-ray crystallography, 2.4 angstroms
A; Molecule type: protein	R; Stec, B.; Teefer, M.M.; Whitlow, M.; Yamano, A.
A; Residues: 483-507, 'E', 509-604 <WII3>	submitted to the Brookhaven Protein Data Bank, June 1995
R; Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.	A; Reference number: A65900; PDB:1KNN
J. Biol. Chem. 244, 3590-3597, 1969	A; Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
A; Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen.	R; Rejante, M.; Llinares, M.
A; Reference number: A92125; MUID:73149248	submitted to the Brookhaven Protein Data Bank, August 1995
A; Contents: annotation; active site	R; Rejante, M.R.; Llinares, M.
R; Trexler, M.; Valli, Z.; Pathy, L.	R; Rejante, M.R.; Llinares, M.
J. Biol. Chem. 257, 7401-7405, 1982	A; Reference number: A65804; PDB:1HK
A; Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.	A; Contents: annotation; conformation by (1)H-NMR, residues 103-181
A; Reference number: A92382; MUID:8221305	R; Rejante, M.R.; Llinares, M.
A; Contents: annotation; omega-aminocarboxylic acid binding sites	Eur. J. Biochem. 221, 929-937, 1994
R; Valli, Z.; Pathy, L.	A; Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
J. Biol. Chem. 259, 13690-13694, 1984	A; Reference number: S43605; MUID:94237157
A; Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin binding.	A; Contents: annotation; conformation by (1)H-NMR, residues 96-184
A; Reference number: A93458; MUID:85054794	R; Rejante, M.R.; Llinares, M.
A; Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site	Eur. J. Biochem. 221, 933-949, 1994
R; Gao, Y.; Ji, R.W.; Davidson, D.; Schellier, J.; Marti, D.; Soehnzel, S.; McCance, S.G.	A; Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen.
J. Biol. Chem. 271, 29461-29467, 1996	A; Reference number: A58817; MUID:94237158
A; Title: Kringle domains of human angiostatin. Characterization of the anti-proliferative activity of angiostatin.	A; Contents: annotation; conformation by (1)H-NMR
A; Reference number: A58811; MUID:97067211	C; Comment: Plasminogen is synthesized by the kidney and is present in plasma and many
A; Contents: annotation	C; Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKH and PIR:FGHUGB).
R; Liijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.	C; Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:THUA2), immediately after the removal of the kringle 5-80, resulting in two chains connected by two disulfide bonds. Without the inhibiting solid tumors.
Biochemistry 37, 4699-4702, 1998	C; Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial conditions.
A; Reference number: A58812; MUID:9548733	C; Comment: Stomelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin.
A; Contents: annotation	C; Genetics:
R; Tulinsky, A.; Mulichak, A.M.	A; Gene: GDB:PIG
submitted to the Brookhaven Protein Data Bank, July 1991	A; Cross-references: GDB:119499; OMIM:173350
A; Reference number: A51341; DBB:1PK4	A; Map position: 6q26-6q27
A; Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454	A; Introns: 17/1, 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1;
R; Tulinsky, A.; Wu, T.P.	C; Function:
submitted to the Brookhaven Protein Data Bank, July 1991	A; Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a
A; Reference number: A51488; PDB:2PK4	process that involves the walls of the graafian follicle; also activates the urokinase-type plasminogen activator.
A; Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454	A; Pathway: fibrinolysis
R; Wu, T.P.; Tulinsky, A.	C; Superfamily: Plasmin; kringle homology; plasminogen-related protein precursor homolog
submitted to the Brookhaven Protein Data Bank, August 1993	C; Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; homolog; plasminogen-related protein precursor homology <PLPH>
A; Reference number: A51911; PDB:1PKR	F; 1-19/Domain: signal sequence #status predicted <SGT>
A; Reference number: A51911; PDB:1PKR	F; 20-81/Domain: plasminogen #status experimental <PRO>
A; Reference number: A51911; PDB:1PKR	F; 82-96/Domain: activation peptide #status experimental <APT>



QY 1 VYLSCKETGNGKNGRTGMSKURGTCOKWSTSPPRSPATRSEGLENYCRPDN 60  
 Db 79 TYLSECKTGNGKNGRTGSKTSGVTCOKWSSPHKPSPEKKPLAGLENYCRPDN 138  
 QY 61 DPGQPCYTPEKRYDQCDILECEECMHCSEGENYKISTMSGLEQAWDSQSHAH 120  
 Db 139 DEKGPWCYTDPETRFDYCIDPECEDECMHCSGEHYGKISKTMGICQSNGSOPHAH 198  
 QY 121 GYIPSKFPNKKNKKYCRNPDRRLPWCFTDPNKRWECDIPRCTTPPSSGPTYCLK 180  
 Db 199 GYLPSKFPNKKNKKYCRNPDRRLPWCFTDPNKRREFCDIPRCTTPPSSGPTYCLK 258  
 QY 181 GTGENTRGNVAVTSGTQHNSAQTHTRPENPCKNIDENYCRNPDCKRAPWCHT 240  
 Db 259 GRGENRTGTVSUTSGTQHNCQWSAQSPHKHNRTPENPCKNLEENYCRNPDGETAPWCYT 318  
 QY 241 TNSQVWIECKIPSCDSS 258  
 Db 319 TDSEVRWVDYCKIPSCGSS 336

RE 4

PLM  
 N;Alternate names: Plasminogen  
 C;Species: Bos Primigenius taurinus (cattle)  
 C;Date: 30-Sep-1987 #sequence\_revision 28-Apr-1995 #text\_change 18-Jun-1999  
 C;Accession: S47046; A25835; I45961; S03736  
 R;Berglund, L.; Andersen, M.D.; Petersen, T.E.  
 submitted to the EMBL Data Library, May 1994

A;Description: Cloning and characterization of the bovine plasminogen cDNA.  
 A;Reference number: S45046  
 A;Accession: S45046  
 A;Molecule type: mRNA  
 A;Cross-references: EMBL:X79402; NID:9494962; PIDN:CAA55939.1; PID:9494963  
 A;Experimental source: Liver  
 A;Note: it is uncertain whether Met-1 or Met-8 is the initiator  
 R;Schaller, J.; Moser, P.W.; Dammerger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick  
 Eur. J. Biochem. 149, 267-278, 1985  
 A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plasm  
 A;Reference number: A25835; MUID:85203906  
 A;Accession: A25835  
 A;Molecule type: protein  
 A;Residues: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>  
 R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.  
 Biochemistry 23, 4241-4251, 1984  
 A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and  
 A;Reference number: 145961; MUID:85023311  
 A;Accession: I45961  
 A;Molecule type: mRNA  
 A;Cross-references: GB:K02935; NID:9163551; PIDN:AAA30714.1; PID:9163552  
 A;Residues: 706-743, 'R', 745-812 <MAL>  
 R;Brunisholz, R.A.; Lernch, P.G.; Schaller, J.; Rickli, E.B.; Lergier, W.; Manneberg, M.;  
 Bloch, 114, 465-470, 1981  
 A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,  
 A;Reference number: S03735; MUID:81212097  
 A;Accession: S03736  
 A;Molecule type: protein  
 A;Residues: 27-83 <BR>  
 C;Function:  
 A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va  
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act  
 A;Pathway: fibrinolysis  
 C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology  
 C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasmin;  
 F1;26-26/Domain: signal sequence #status predicted<SIC>  
 F;8-03/Domain: plasminogen-related protein precursor homology <PLRH>  
 F;27-812/Domain: plasminogen #status experimental <PRO>  
 F;27-103/Domain: activation peptide #status experimental <APT>  
 F;104-583, 584-812/Domain: plasmin #status experimental <MAT>  
 F;104-583/Domain: plasmin chain A #status experimental <ACH>

Query Match 83.8%; Score 1291; DB 1; Length 812;  
 Best Local Similarity 80.8%; Pred. No. 4.9e-87; Mismatches 27; Indels 0; Gaps 0;  
 Matches 210; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

RE 5

PLM  
 N;Alternate names: Plasminogen  
 C;Species: Mus musculus (house mouse)  
 C;Date: 20-Sep-1991 #sequence\_revision 01-Nov-1996 #text\_change 18-Jun-1999  
 C;Accession: A38544; S48202; S44203  
 R;Beggen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.  
 Genomics 8, 49-61, 1990  
 A;Title: Characterization of the cDNA coding for mouse plasminogen and localization o  
 A;Reference number: A38514; MUID:91184812  
 A;Accession: A38514  
 A;Molecule type: mRNA  
 A;Residues: 1-812 <DE>  
 A;Cross-references: GB:J04766; NID:9200402; PIDN:AAA50168.1; PID:9200403  
 R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.  
 Eur. J. Biochem. 224, 863-871, 1994  
 A;Title: Characterization of the murine plasma fibrinolytic system.  
 A;Reference number: S48202; MUID:95010076  
 A;Accession: S48202  
 A;Molecule type: protein  
 A;Residues: 20-23 <LI>  
 A;Accession: S48203  
 A;Molecule type: protein  
 A;Residues: 22-27 <LI>  
 C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many  
 C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plas  
 meditately after dissociation from the clot. In the presence of the inhibitor, the act  
 e inhibitor, the activation involves also removal of the activation peptide.  
 C;Comment: Stromeysin 1 (see PIR:KCM51) acts on plasminogen to produce angiostatin.  
 C;Function:  
 A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a  
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen

A: Pathway: fibrinolysis  
 C: Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolase; plasma protein; protease inhibitor; protein precursor homology  
 F: 1-1975/Domain: plasminogen-related protein precursor homology <PLPH>  
 F: 20-812/Domain: plasminogen #status predicted  
 F: 20-967/Domain: actin-binding peptide #status predicted <APT>  
 F: 79-466/Product: angiotensin #status predicted <AST>  
 F: 97-581,582-812/Product: plasmin #status predicted <MAT>  
 F: 97-581/Domain: signal sequence #status predicted <SIG>  
 F: 103-181/Domain: chain A #status predicted <ACH>  
 F: 185-262/Domain: kringle homology <KR1>  
 F: 275-352/Domain: kringle homology <KR2>  
 F: 377-454/Domain: kringle homology <KR3>  
 F: 481-560/Domain: kringle homology <KR4>  
 F: 582-812/Domain: chain B #status predicted <BCB>  
 F: 582-805/Domain: trypsin homology <TRX>  
 F: 49-73, 53-61, 103-181, 124-164, 152-176, 185-262, 188-316, 206-245, 234-257, 275-352, 296-335, 324-360/Binding site: Glu-Asn (stromelysin 1) #status predicted  
 F: 466-467/Cleavage site: Thr-val (stromelysin 1) #status predicted  
 F: 581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental  
 F: 624, 667, 672/Active site: His, Asp, Ser #status predicted

**b** F: 1-1975/Domain: status predicted  
 F: 1-1975/Cleavage site: Glu-Asn (stromelysin 1) #status predicted  
 F: 1-1975/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F: 466-467/Cleavage site: Thr-val (stromelysin 1) #status predicted  
 F: 581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental  
 F: 624, 667, 672/Active site: His, Asp, Ser #status predicted

**RESULT** 6

I46260  
 plasmin (EC 3.4.21.7) precursor - western European hedgehog  
 C:Species: *Erinaceus europaeus* (western European hedgehog)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 16-Jul-1999  
 C:Accession: I46260  
 R:Lawn, R.M.; Boenmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong, J. Biol. Chem. 270, 24004-24009, 1995  
 A:Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein A: Reference number: I46259; MUID:9602778  
 A:Accession: I46260  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Residues: 1-810 <LAL>  
 A:Cross-references: EMBL:U33171; NID:Q1046360; PID:gi1046361  
 C:Keywords: hydrolase; serine proteinase  
 C:Superfamily: plasmin; kringle homology; Plasminogen-related protein precursor homology  
 C:Keywords: hydrolase; serine proteinase  
 C:Cross-references: EMBL:U33171; NID:Q1046360; PID:gi1046361  
 F:1-967/Domain: plasminogen-related protein precursor homology <PLPH>  
 F:103-181/Domain: kringle homology <KR1>  
 F:185-262/Domain: kringle homology <KR2>  
 F:275-352/Domain: kringle homology <KR3>  
 F:379-456/Domain: kringle homology <KR4>

Query Match 80.3%; Score 1237; DB 2; Length 810;  
 Best Local Similarity 77.9%; Pred. No. 4.3e-83; Mismatches 31; Indels 0; Gaps 0;  
 Matches 201; Conservative 26; MisMatch 31; Index 0; Gaps 0;  
 QY 1 VYLSECKTGCKNGKNYGTGMSKTKNGTICQWSSSPHRPRFSPATHPSCELEENYCRNPDN 60  
 Db 98 MYLSECKVGKNGKYYGTGVSQKTKGTLGTCQWSSAETPHKPKPSDPENPSEGIDQNYCRNPDN 157  
 QY 61 DPOGMCYTIDPEKKYDCCILEGECHCMSGENDGKISKTMGLEGQWMSQSPH 120  
 Db 158 DPKGPWCYTIDPEPVRYEYCETIQCEDECMHCSGONYVGKISRTMSGLEQWMSQSPH 217  
 QY 121 GYIPSKFPKPKNLKKNNYCRNFDRELPCFTIDPNKRWECDIPRCTTPPPSSGPTYQICK 180  
 Db 218 GPKSKFPKPKNLKKNNYCRNFDRELPCFTIDPNKRWECDIPRCTTPPPSSGPTYQICK 277  
 QY 181 GTGENTGRNVAVTWSGHTCQWSSAQTPHTERTPENPCKNLDENYCRPDKGPKAWPH 240  
 Db 278 GNGEHYQGNNVAVTWSGLTCQWMSQPHDRTPENPCKNLDENYCRPDKGPKAWPH 337  
 QY 241 TNSQWYECKIPSDSS 258  
 Db 338 TNSSVRWECKIPDCVSS 355

RESULT 7

T18518 apolipoprotein(a) - western European hedgehog (fragment)  
 C;Species: *Erinaceus europaeus* (western European hedgehog)  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 07-dec-1999  
 C;Accession: T18518  
 R;Lawn, R.M.; Bookmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; F  
 J. Biol. Chem., 270, 24004-24009, 1995  
 A;Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipop  
 A;Reference number: 146259; MUID: 96025778  
 A;Accession: T18518  
 A;Status: Preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-2869 <LAW>  
 A;Cross-references: EMBL:U33170; NTD:gi046359; PID:gi046359; PID:AC48522.1  
 A;Experimental source: liver  
 A;Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis,  
 ent apolipoprotein(a).

Query Match 57.2%; Score 881; DB 2; Length 2869;  
 Best Local Similarity 55.0%; Pred. No. 1.5e-56; Mismatches 149; Conservative 36; Indels 16; Gaps 3; Matches 149; MisMatch 149; Index 0; Gaps 3;

QY 3 LSECKTGCKNGKNYGTGMSKTKNGTICQWSSSPHRPRFSPATHPSCELEENYCRNPDN 62  
 Db 2495 VDQCLCETGTYEYRGNMMAVTASGHTCQWRIQSPHSHRSPENYPIKNUGNYCRNPDG 2553  
 QY 63 OGPWCYTIDPEPKRYDCCIFCE-----EECHCMSGENDGKISKTMGLEGQWMSQSPH 110  
 Db 2554 VAPWCYTTSAMRWEYCSIFACESSTPPTEBLVVPWQECILEGGENYQGMINAIVVGOPCQ 2613  
 QY 111 AWDSOSPHAKGKYPISKEPKNLKKNNYCRNFDRELPCFTIDPNKRWECDIPRCTTPP 170  
 Db 2614 GWRKQPKPRHETPYTENPYSKPNLFGNYCRNFDRELPCFTIDPNKRWECDIPRCTTPP 2673  
 QY 171 SSGPTY--QCLKGTYENYGRNVAVTWSGHTCQWSSAQTPHTERTPENPCKNLDENYCR 227  
 Db 2674 PTEPMKIPDOCLEGTYENYGRNVAVTWSGHTCQWSSAQTPHTERTPENPCKNLDENYCR 2733  
 QY 228 RNPDGKRAWPWCHTTSNQVWEYCKIPSCDS 258  
 Db 2734 RNPDGKRAWPWCHTTSNQVWEYCKIPSCNS 2764

RESULT 8

JH0579 hepatocyte growth factor precursor [validated] - human

N;Alternate names: hepatoprotein A; scatter factor

C;Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 08-Dec-2000

C;Accession: JH0579; JU0333; A41140; B36677; A35512; A39006; PH0114; A37796; S06

R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.

Gene 102, 213-219, 1991

A;Title: Organization of the human hepatocyte growth factor-encoding gene.

A;Reference number: JH0579; MUID:91340155

A;Accession: JH0579

A;Molecule type: DNA

A;Residues: 1-128 <SFR>

A;Cross-references: DDBJ:D90318

A;Note: the authors translated the codon GAA for residue 662 as GLY

R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.

submitted to JRPID, March 1991

A;Reference number: JU0333

A;Accession: JU0333

A;Molecule type: DNA

A;Residues: 1-1481; RP' 484-728 <SE2>

R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.

Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991

A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor

A;Reference number: A41140; MUID:91334393

A;Molecule type: mRNA

A;Residues: 1-128 <WII>

A;Cross-references: GB:MT3239; NID:9337935; PIDN:AAA64339.1; PID:9337936

R;Seki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.

Biochem. Biophys. Res. Commun. 172, 321-327, 1990

A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor

A;Reference number: A36677; MUID:91025062

A;Accession: B46677

A;Molecule type: mRNA

A;Residues: 1-728 <SE3>

A;Cross-references: GB:MG60718; NID:9184031; PIDN:AAA52648.1; PID:9184032

A;Accession: A46677

A;Molecule type: mRNA

A;Residues: 1-161,167-728 <SE4>

A;Cross-references: EMBL:X16323

A;Experimental source: leukocyte

R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya, M.

Biochem. Biophys. Res. Commun. 163, 967-973, 1989

A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factor

A;Reference number: A33512; MUID:89392017

A;Accession: A33512

A;Residues: 1-728 <M1Y>

A;Cross-references: GB:MG29145; NID:9184041; PIDN:AAA52650.1; PID:9306846

R;Rubb, J.S.; Chan, A.M.L.; Botta, D.P.; Burgess, W.H.; Taylor, W.G.; Czech, A.C.; Hirsh, Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991

A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocyte growth factor

A;Reference number: A39006; MUID:91110540

A;Accession: A39006

A;Molecule type: mRNA

A;Residues: 1-161,167-728 <RUB>

A;Cross-references: GB:MG5379

A;Experimental source: embryonic lung

R;Yoshiyama, T.; Arakaki, N.; Naka, D.; Takahashi, K.; Hiroto, S.; Kondo, J.; Nakayama, M.

Biochem. Biophys. Res. Commun. 175, 660-667, 1991

A;Title: Identification of the N-terminal residue of the heavy chain of both native and

A;Reference number: PH0114; MUID:91207365

A;Accession: PH0114

A;Molecule type: protein

A;Residues: 32-43;53-58 <XOS>

A;Experimental source: plasma

R;Weidner, K.M.; Berens, J.; vanderkerckhove, J.; Bircheimer, W.

J. Cell Biol. 111, 2097-2108, 1990

A;Title: Scatter factor: molecular characteristics and effect on the invasiveness of

A;Reference number: A37796; MUID:91035621

A;Accession: A37796

A;Molecule type: protein

A;Residues: 86-91;329-344;356-363, 'XX', 366-370;425-434;442-447, 'X',449-450;543-546, 'X'

Nature 342, 440-443, 1989

R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimomishi, M.; Sugimura, A.; Ta

R;Hartmann, G.; Naldini, L.; Widner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Bir

Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992

A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth factor

A;Accession number: 159214; MUID:93087571

A;Title: A preliminary: translated from GB/EMBL/DBJ

A;Accession: 159214

A;Molecule type: mRNA

A;Residues: 1-288; RP' <HAR>

A;Cross-references: GB:L02931; NID:9184033; PIDN:AAA52649.1; PID:9184034

R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.

Eur. J. Biochem. 197, 15-22, 1991

A;Title: An alternatively processed mRNA generated from human hepatocyte growth factor

A;Reference number: S15443; MUID:91200041

A;Accession: S15443

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-288; ET' <HAR>

A;Cross-references: GB:L02931; NID:9184033; PIDN:AAA52649.1; PID:9184034

R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.

Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991

A;Title: tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cDNA

A;Accession number: 152253; MUID:92062058

A;Title: A preliminary: translated from GB/EMBL/DBJ

A;Accession: 152253

A;Molecule type: mRNA

A;Residues: 161-166 <SHI>

A;Cross-references: GB:S62561; NID:9237956; PIDN:AB20169.1; PID:9237997

A;Gene: GB:HGF

A;Cross-references: GDB:127524; OMIM:142409

A;Map position: 7q21.1-7q21.1

A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1;

C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor

A;Function:

A;Description: stimulates mitosis of hepatocytes and other cells

A;Note: does not have protease activity

C;Keywords: alternative splicing; hepatocyte growth factor; kringle homology; growth factor; heterodimer; kringle; F1-31;Domain: signal sequence #status predicted <SSG>

F1-32-49, 49-728;product: hepatocyte growth factor #status experimental <MAT>

F1-32-494/Domain: alpha chain #status experimental <ACH>

F1-218-206/Domain: kringle homology <KR1>

F1-211-288/Domain: kringle homology <KR2>

F1-305-383/Domain: kringle homology <KR3>

F1-391-469/Domain: kringle homology <KR4>

F1-495-728/Domain: beta chain #status experimental <BCH>

F1-495-716/Domain: trypsin homology <TRY>

F1-32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

F1-294-402,506, 653/Binding site: carbohydrate (Asn) (covalent) #status predicted

F1-487-604/Disulfide bonds: #status predicted

Query Match 51.8%; Score 797; DB 1; Length 728;

Best Local Similarity 51.0%; Pred. No. 5.5e-51;

Matches 134; Conservative 42; Mismatches 81; Indels 6; Gaps 4;

OY 2 YLSECKTGNGKNYRGMSKTRNGITCQRWSSTSPHRPRSPATHPSEGLEENYCRNPND 61





Query Match	49.8%	Score	766.5	DB	1	Length	716
Best Local Similarity	48.5%	Pred. No.	9.2e-49				
Matches	132;	Conservative	36;	Mismatches	89;	Indels	15;
						Gaps	5;
C; Species:	Mus musculus (house mouse)						
C; Alternate names:	hepatocyte growth factor-like protein						
C; Date:	17-Jul-1992	#sequence_revision	17-Jul-1992	#text_change	18-Jun-1999		
C; Accession:	A40332;	B40332					
R; Degen, S. J. F.; Stuart, L. A.; Han, S.; Jamison, C. S.							
Biochemistry	30,	9781-9791,	1991				
A; Title:	Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor-like protein						
A; Reference number:	A40332;	MUID:	9202017				
A; Accession number:	A40332						
A; Molecule type: DNA							
A; Residues:	1-716 <DEG>						
A; Accession:	GB:M74180;	NID:	9193831;	PIDN:	AAA50166.1;	PID:	9193832
A; Molecule type: mRNA							
A; Residues:	1-18;	P'	20-716 <DEG2>				
A; Cross-references:	GB:M74181;	NID:	9193833;	PIDN:	AAA50167.1;	PID:	9193834
C; Genomics:							
A; Introns:	18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1;						
C; Complex:	disulfide-bonded heterodimer of chains derived from the same precursor						
C; Superfamily:	hepatocyte growth factor; kringle homology						
C; Keywords:	duplication; glycoprotein; growth factor; kringle						
F; 1-31/Domain:	signal sequence	#status predicted	<SIC>				
F; 19-433/Domain:	alpha chain	#status experimental	<ACH>				
F; 110-186/Domain:	kringle homology	<KR1>					
F; 191-268/Domain:	kringle homology	<KR2>					
F; 292-370/Domain:	kringle homology	<KR3>					
F; 379-457/Domain:	kringle homology	<KR4>					
F; 484-711/Domain:	beta chain	#status experimental	<BCB>				
F; 489-709/Domain:	trypsin homology	<TR1>					
F; 72,173,305,620/Binding site:	carbohydrate (Asn)	(covalent)	#status predicted				
A; Title:	A role for HGF/SF in neural induction and its expression in Hensen's node during						
A; Reference number:	151285;	MUID:	95237013				
A; Accession:	151285						
A; Status:	preliminary; translated from GB/EMBL/DBJ						
A; Molecule type:	mRNA						
A; Residues:	1-411 <STR>						
Cross-references:	GB:S77480;	NID:	998675;	PID:	998676		
Superfamily:	hepatocyte growth factor; kringle homology; trypsin homology						
Accession:	151285						
Date:	13-Sep-1996	#sequence_revision	13-Sep-1996	#text_change	16-Jul-1999		
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F; 1965-2043/Domain: kringle homology <KR118>  
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F; 2878-2955/Domain: kringle homology <KR26>  
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F; 4328-4541/Domain: trypsin homology <TRX>

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Qy	63	QGPWCYTDTDEKKYQDCIEE-----	-----	EECM 89
Db	3839	R-PWCYTMDPSYRVWENLQ:-----	-----	3897
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Db	3898	RGDGOSYRGTLSTTITGRICQSWSSMTPHWRHRRIPLYPNAGLJTRNYCRNPDAEIRPWCY	3957	
Qy	150	ITDPNKRWECDIPIRG-----TTP-----	-----	PPSSGTYQ-CLKGIGEN 185
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Qy	186	YRGNVATVYQHTGHSWADQPHERTPHTNPKNDNLYCRNPDGRKPAQHHTNSQV	245	
Db	4018	YRGISSTTIVGRTCSWSSMIPWHQRTPEBNYPNAGLTIENYCRNPDSQKQPWCYTDPVC	4077	
Qy	246	RWEYKIPSDSS	258	
Db	4078	RWEYCNLTQSET	4090	



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